

Trans-Sialidases-WO ST25.txt
SEQUENCE LISTING

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<120> Trans-Sialidases obtained from Trypanosoma congolense

<130> NUT-047-WO

<150> DE 10258400.1

<151> 2002-12-13

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1491

<212> DNA

<213> Trypanosoma congolense

<220>

<221> CDS

<222> (1)..(1491)

<223>

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agg gag gtt ata att ccg aat ggt cgt gtg gat gcc cac tac tcc cgc	96
Arg Glu Val Ile Ile Pro Asn Gly Arg Val Asp Ala His Tyr Ser Arg	
20 25 30	
gtc gtt gat ccc act gtt gtt gcg aag ggt aat aac att tat gtt ctc	144
Val Val Asp Pro Thr Val Val Ala Lys Gly Asn Asn Ile Tyr Val Leu	
35 40 45	
gtt ggg cgg tac aat gtc acg cgg ggc tac tgg cac aat agg aac aac	192
Val Gly Arg Tyr Asn Val Thr Arg Gly Tyr Trp His Asn Arg Asn Asn	
50 55 60	
aag gct ggc ata gcc gat tgg gag ccc ttc gtg tac aag ggc acg gtg	240
Lys Ala Gly Ile Ala Asp Trp Glu Pro Phe Val Tyr Lys Gly Thr Val	
65 70 75 80	
aac gtg ggc acg aag ggc aat gcc act gat gtg tcg atc agc tgg gag	288
Asn Val Gly Thr Lys Gly Asn Ala Thr Asp Val Ser Ile Ser Trp Glu	
85 90 95	
agg act gca ctg aag tcg ctg tac aac ttc ccg gtt tcg gga agc cct	336
Arg Thr Ala Leu Lys Ser Leu Tyr Asn Phe Pro Val Ser Gly Ser Pro	
100 105 110	
ggc acg cag ttc ctt gga ggg gct ggg ggt ggt gtt gta aca tcc aac	384
Gly Thr Gln Phe Leu Gly Gly Ala Gly Gly Gly Val Val Thr Ser Asn	
115 120 125	

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ggg Gly	acg Thr 130	att Ile	gtg Val	ctg Leu	cca Pro	gtg Val 135	cag Gln	gca Ala	agg Arg	aac Asn	aag Lys 140	gcc Ala	aac Asn	cgt Arg	gtt Val	432
gtg Val 145	agc Ser	atg Met	atc Ile	ctg Leu	tac Tyr 150	tcg Ser	gct Ala	gac Asp	gat Asp	gga Gly 155	aag Lys	tca Ser	tgg Trp	cac His	ttt Phe 160	480
ggg Gly	aag Lys	ggt Gly	gag Glu 165	gcc Ala 165	ggt Gly	gta Val	ggc Gly	acg Thr 170	tcc Ser	gag Glu	gct Ala	gcc Ala	ctc Leu	act Thr 175	gag Glu	528
tgg Trp	gac Asp	ggc Gly	aag Lys 180	ctg Leu	ctg Leu	att Ile	agt Ser	gca Ala 185	cga Arg	tcc Ser	gat Asp	ggt Gly	gga Gly 190	cag Gln	ggc Gly	576
tac Tyr	cgc Arg	atg Met 195	ata Ile	ttc Phe	gaa Glu	tcg Ser	agt Ser 200	gac Asp	ctt Leu	ggt Gly	gcg Ala	acg Thr 205	tgg Trp	aaa Lys	gag Glu	624
atg Met 210	ctc Leu	aac Asn	agc Ser	atc Ile	tcc Ser	cgc Arg 215	gtg Val	att Ile	ggc Gly	aac Asn	tct Ser 220	ccg Pro	ggt Gly	cgc Arg	agt Ser	672
ggt Gly 225	cct Pro	ggc Gly	agc Ser	tcg Ser 230	agt Ser	ggc Gly	ttc Phe	atc Ile	acg Thr	gtg Val 235	aca Thr	gtg Val	gag Glu	ggt Gly	gtg Val 240	720
cct Pro	gtg Val	atg Met	ctg Leu	att Ile 245	acc Thr	cac His	ccg Pro	aag Lys	aac Asn 250	ctt Leu	aag Lys	ggc Gly	tcg Ser	tat Tyr 255	tat Tyr	768
cgg Arg	gac Asp	cgt Arg	ctg Leu 260	cag Gln	ctg Leu	tgg Trp	atg Met	acg Thr 265	gac Asp	ggc Gly	aat Asn	cgt Arg	atg Met 270	tgg Trp	cat His	816
gtc Val	ggg Gly	cag Gln 275	gtc Val	tct Ser	gag Glu	ggc Gly	gac Asp 280	gat Asp	aac Asn	agc Ser	gct Ala	tac Tyr 285	agc Ser	tcc Ser	ctg Leu	864
ctg Leu	tac Tyr 290	act Thr	ccg Pro	gac Asp	ggg Gly	gtc Val 295	ctg Leu	tac Tyr	tgc Cys	ttg Leu	cat His 300	gag Glu	cag Gln	aac Asn	att Ile	912
gat Asp 305	gag Glu	gtg Val	tac Tyr	agc Ser	ctc Leu 310	cac His	ctt Leu	gtg Val	cgc Arg	ctt Leu 315	gtg Val	gac Asp	gag Glu	ctg Leu	aaa Lys 320	960
agc Ser	att Ile	aaa Lys	tca Ser 325	acg Thr	gct Ala	ctg Leu	gtg Val	tgg Trp	aag Lys 330	gca Ala	cag Gln	gac Asp	gag Glu	ctt Leu 335	ctc Leu	1008
ctg Leu	ggc Gly	aac Asn	tgc Cys 340	ctc Leu	ccg Pro	ggc Gly	gat Asp	aaa Lys 345	tac Tyr	gat Asp	ccc Pro	ggg Gly	tgt Cys 350	gac Asp	ggc Gly	1056
atc Ile	ccc Pro	acc Thr 355	gct Ala	ggg Gly	ctt Leu	gcc Ala	ggg Gly 360	ctg Leu	ctg Leu	gta Val	gga Gly	ccc Pro	ctg Leu	acg Thr	gag Glu	1104
aag Lys	acg Thr	tgg Trp	ccc Pro	gac Asp	gcg Ala	tat Tyr	cgg Arg	tgc Cys	gtg Val	aac Asn	gct Ala	gca Ala	acc Thr	agc Ser	ggc Gly	1152

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370	375	380	
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gct Ala 390	gaa Glu	ggc Gly	gtg Val
cgg Arg	ctg Leu	gac Asp 395	gtg Val
ggt Gly	ggc Gly	ggt Gly	ggc Gly 400
1200			
cat His	gtt Val	gtg Val	tgg Trp
ccc Pro 405	gtg Val	agt Ser	gag Glu
cag Gln 410	ggg Gly	cag Gln	gac Asp
cag Gln	arg Arg	ggt Gly	tac Tyr 415
1248			
ttt Phe	acc Thr	aac Asn	agc Ser 420
gag Glu	ttc Phe	acg Thr	ctc Leu
gcc Ala 425	gtc Val	acg Thr	gtg Val
cgg Arg	ttt Phe	gac Asp 430	gag Glu
1296			
atg Met	cca Pro	cgg Arg 435	ggg Gly
gag Glu	ctc Leu	ccg Pro	ttg Leu 440
ctg Leu	ggg Gly	ttt Phe	gtg Val
aac Asn 445	cgc Arg	aaa Lys	ggg Gly
1344			
aag Lys	gtg Val 450	aag Lys	aag Lys
ata Ile	ctg Leu	aag Lys 455	gtg Val
tcg Ser	ctg Leu	agc Ser	ggg Gly 460
gtg Val	gag Glu	tgg Trp	ctc Leu
1392			
ctg Leu 465	gca Ala	tac Tyr	ggg Gly
aat Asn	gag Glu 470	tac Tyr	aac Asn
agc Ser	aca Thr	gcc Ala 475	gct Ala
gag Glu	ccg Pro	ctg Leu	gac Asp 480
1440			
gtg Val	aac Asn	gag Glu	agc Ser
cac His 485	cag Gln	gtg Val	gtg Val
cta Leu	gcg Ala 490	ctt Leu	cac His
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tcc Ser			
1491			

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Val	Val	Asp 35	Pro	Thr	Val	Val	Ala 40	Lys	Gly	Asn	Asn	Ile 45	Tyr	Val	Leu
Val	Gly 50	Arg	Tyr	Asn	Val	Thr 55	Arg	Gly	Tyr	Trp	His 60	Asn	Arg	Asn	Asn
Lys 65	Ala	Gly	Ile	Ala 70	Asp	Trp	Glu	Pro	Phe 75	Val	Tyr	Lys	Gly	Thr	Val 80
Asn	Val	Gly	Thr	Lys	Gly	Asn	Ala	Thr	Asp	Val	Ser	Ile	Ser	Trp	Glu

Arg Thr Ala Leu Lys Ser Leu Tyr Asn Phe Pro Val Ser Gly Ser Pro
 100 105 110

Gly Thr Gln Phe Leu Gly Gly Ala Gly Gly Gly Val Val Thr Ser Asn
 115 120 125

Gly Thr Ile Val Leu Pro Val Gln Ala Arg Asn Lys Ala Asn Arg Val
 130 135 140

Val Ser Met Ile Leu Tyr Ser Ala Asp Asp Gly Lys Ser Trp His Phe
 145 150 155 160

Gly Lys Gly Glu Ala Gly Val Gly Thr Ser Glu Ala Ala Leu Thr Glu
 165 170 175

Trp Asp Gly Lys Leu Leu Ile Ser Ala Arg Ser Asp Gly Gly Gln Gly
 180 185 190

Tyr Arg Met Ile Phe Glu Ser Ser Asp Leu Gly Ala Thr Trp Lys Glu
 195 200 205

Met Leu Asn Ser Ile Ser Arg Val Ile Gly Asn Ser Pro Gly Arg Ser
 210 215 220

Gly Pro Gly Ser Ser Ser Gly Phe Ile Thr Val Thr Val Glu Gly Val
 225 230 235 240

Pro Val Met Leu Ile Thr His Pro Lys Asn Leu Lys Gly Ser Tyr Tyr
 245 250 255

Arg Asp Arg Leu Gln Leu Trp Met Thr Asp Gly Asn Arg Met Trp His
 260 265 270

Val Gly Gln Val Ser Glu Gly Asp Asp Asn Ser Ala Tyr Ser Ser Leu
 275 280 285

Leu Tyr Thr Pro Asp Gly Val Leu Tyr Cys Leu His Glu Gln Asn Ile
 290 295 300

Asp Glu Val Tyr Ser Leu His Leu Val Arg Leu Val Asp Glu Leu Lys
 305 310 315 320

Ser Ile Lys Ser Thr Ala Leu Val Trp Lys Ala Gln Asp Glu Leu Leu
 325 330 335

Trans-Sialidases-WO ST25.txt

Leu Gly Asn Cys Leu Pro Gly Asp Lys Tyr Asp Pro Gly Cys Asp Gly
340 345 350

Ile Pro Thr Ala Gly Leu Ala Gly Leu Leu Val Gly Pro Leu Thr Glu
355 360 365

Lys Thr Trp Pro Asp Ala Tyr Arg Cys Val Asn Ala Ala Thr Ser Gly
370 375 380

Ala Val Ser Thr Ala Glu Gly Val Arg Leu Asp Val Gly Gly Gly Gly
385 390 395 400

His Val Val Trp Pro Val Ser Glu Gln Gly Gln Asp Gln Arg Tyr Tyr
405 410 415

Phe Thr Asn Ser Glu Phe Thr Leu Ala Val Thr Val Arg Phe Asp Glu
420 425 430

Met Pro Arg Gly Glu Leu Pro Leu Leu Gly Phe Val Asn Arg Lys Gly
435 440 445

Lys Val Lys Lys Ile Leu Lys Val Ser Leu Ser Gly Val Glu Trp Leu
450 455 460

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Val Asn Glu Ser His Gln Val Val Leu Ala Leu His Asp Gly Ile Val
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<210> 3
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<212> DNA
<213> Trypanosoma congolense

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Phe Asp Thr Arg Tyr Leu Arg Ala Ser Asp Ser Ser Leu Ile Asp Thr
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Ile Ile Lys Asn Ala Arg Leu Thr Asp Asn Phe Ser Arg Val Val Asp		
50 55 60		
cca acg gtt gtt gtt aag ggt gat aac ttg ttt att ttt gtt ggg agg	240	
Pro Thr Val Val Val Lys Gly Asp Asn Leu Phe Ile Phe Val Gly Arg		
65 70 75 80		
tac aac acc tca tct gcc cca tgg gtc tgg cag gaa aac ggt aaa gac	288	
Tyr Asn Thr Ser Ser Ala Pro Trp Val Trp Gln Glu Asn Gly Lys Asp		
85 90 95		
tgg gat gta ctg ttg tac aag gcc aag gtg agg aag gaa tca gcg ggt	336	
Trp Asp Val Leu Tyr Lys Ala Lys Val Arg Lys Glu Ser Ala Gly		
100 105 110		
ggg gta cca tca gtg agc ttt aca tgg gac gaa ccc cta tac ctg aag	384	
Gly Val Pro Ser Val Ser Phe Thr Trp Asp Glu Pro Leu Tyr Leu Lys		
115 120 125		
cat ctg ctc acc tct gtc ggt aaa ata gac ggc agg tcc ctc ata caa	432	
His Leu Leu Thr Ser Val Gly Lys Ile Asp Gly Arg Ser Leu Ile Gln		
130 135 140		
tac att ggt ggc gtt gga aat ggt att gta aca ccg aaa ggt act atc	480	
Tyr Ile Gly Gly Val Gly Asn Gly Ile Val Thr Pro Lys Gly Thr Ile		
145 150 155 160		
gtg ttt cca gtt cag gtt tta aac acc aac aaa tcc gtc atg aac atg	528	
Val Phe Pro Val Gln Val Leu Asn Thr Asn Lys Ser Val Met Asn Met		
165 170 175		
ctt ctg tat tca agt aac gac gga aaa acc tgg gag ttc agc aaa act	576	
Leu Leu Tyr Ser Ser Asn Asp Gly Lys Thr Trp Glu Phe Ser Lys Thr		
180 185 190		
tcc aca ccc gcg ggc aca act gag gcc tcc ctt gtt tgg tgg gat gga	624	
Ser Thr Pro Ala Gly Thr Thr Glu Ala Ser Leu Val Trp Trp Asp Gly		
195 200 205		
caa cta ctt ctc aca agc aga aca act ccg gat gtc ggc agc cgc aaa	672	
Gln Leu Leu Leu Thr Ser Arg Thr Thr Pro Asp Val Gly Ser Arg Lys		
210 215 220		
gta tat tta aca agc gac ctc gga act tca tgg aat gaa gcg atc gga	720	
Val Tyr Leu Thr Ser Asp Leu Gly Thr Ser Trp Asn Glu Ala Ile Gly		
225 230 235 240		
agt atc tct cgt gta att ggt aac tcg cgg tac cgt aac gat cct ggg	768	
Ser Ile Ser Arg Val Ile Gly Asn Ser Arg Tyr Arg Asn Asp Pro Gly		
245 250 255		
ggg tca ggt agc tca att gcc ata act gtg gag gga gta ccg gtg atg	816	
Gly Ser Gly Ser Ser Ile Ala Ile Thr Val Glu Gly Val Pro Val Met		
260 265 270		
ctg att acc cac ccg	831	
Leu Ile Thr His Pro		
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Trans-Sialidases-WO ST25.txt

<210> 4
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 <213> Trypanosoma congolense

<400> 4

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 35 40 45

Ile Ile Lys Asn Ala Arg Leu Thr Asp Asn Phe Ser Arg Val Val Asp
 50 55 60

Pro Thr Val Val Val Lys Gly Asp Asn Leu Phe Ile Phe Val Gly Arg
 65 70 75 80

Tyr Asn Thr Ser Ser Ala Pro Trp Val Trp Gln Glu Asn Gly Lys Asp
 85 90 95

Trp Asp Val Leu Leu Tyr Lys Ala Lys Val Arg Lys Glu Ser Ala Gly
 100 105 110

Gly Val Pro Ser Val Ser Phe Thr Trp Asp Glu Pro Leu Tyr Leu Lys
 115 120 125

His Leu Leu Thr Ser Val Gly Lys Ile Asp Gly Arg Ser Leu Ile Gln
 130 135 140

Tyr Ile Gly Gly Val Gly Asn Gly Ile Val Thr Pro Lys Gly Thr Ile
 145 150 155 160

Val Phe Pro Val Gln Val Leu Asn Thr Asn Lys Ser Val Met Asn Met
 165 170 175

Leu Leu Tyr Ser Ser Asn Asp Gly Lys Thr Trp Glu Phe Ser Lys Thr
 180 185 190

Ser Thr Pro Ala Gly Thr Thr Glu Ala Ser Leu Val Trp Trp Asp Gly
 195 200 205

Gln Leu Leu Leu Thr Ser Arg Thr Thr Pro Asp Val Gly Ser Arg Lys
 210 215 220

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Val Tyr Leu Thr Ser Asp Leu Gly Thr Ser Trp Asn Glu Ala Ile Gly
225 230 235 240

Ser Ile Ser Arg Val Ile Gly Asn Ser Arg Tyr Arg Asn Asp Pro Gly
245 250 255

Gly Ser Gly Ser Ile Ala Ile Thr Val Glu Gly Val Pro Val Met
260 265 270

Leu Ile Thr His Pro
275